

<110> Adams, John W
Connolly, Daniel T

<120> Human G Protein-Coupled Receptor and Modulators Thereof For the
Treatment of Cardiovascular Disorders

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<151> 2003-06-20

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Arg Ala His Leu Asn Ser Leu Arg Phe Pro Val Gln Gly Asn Gly Thr
85 90 95

Asp Ile Leu Ser Met Ala Met Thr Thr Val Cys Thr Pro Thr Gly Asn
100 105 110

Asp Leu Leu Cys Phe Cys Glu Lys Gly Tyr Gln Trp Pro Glu Glu Arg
115 120 125

Cys Leu Ser Ser Leu Thr Cys Gln Glu His Asp Ser Ala Leu Pro Gly
130 135 140

Arg Tyr Cys Asn Cys Leu Lys Gly Leu Pro Pro Gln Gly Pro Phe Cys
145 150 155 160

Gln Leu Pro Glu Thr Tyr Ile Thr Leu Lys Ile Lys Val Arg Leu Asn
165 170 175

Ile Gly Phe Gln Glu Asp Leu Glu Asn Thr Ser Ser Ala Leu Tyr Arg
180 185 190

Ser Tyr Lys Thr Asp Leu Glu Arg Ala Phe Arg Ala Gly Tyr Arg Thr
195 200 205

Leu Pro Gly Phe Arg Ser Val Thr Val Thr Gln Phe Thr Lys Gly Ser
210 215 220

Val Val Val Asp Tyr Ile Val Glu Val Ala Ser Ala Pro Leu Pro Gly
225 230 235 240

Ser Ile His Lys Ala Asn Glu Gln Val Ile Gln Asn Leu Asn Gln Thr
245 250 255

Tyr Lys Met Asp Tyr Asn Ser Phe Gln Gly Thr Pro Ser Asn Glu Thr
260 265 270

Lys Phe Thr Val Thr Pro Glu Phe Ile Phe Glu Gly Asp Asn Val Thr
275 280 285

Leu Glu Cys Glu Ser Glu Phe Val Ser Ser Asn Thr Ser Trp Phe Tyr
290 295 300

Gly Glu Lys Arg Ser Asp Ile Gln Asn Ser Asp Lys Phe Ser Ile His
305 310 315 320

Thr Ser Ile Ile Asn Asn Ile Ser Leu Val Thr Arg Leu Thr Ile Phe
325 330 335

60.US2.PCT.txt

Asn Phe Thr Gln His Asp Ala Gly Leu Tyr Gly Cys Asn Val Thr Leu
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Asp Ile Phe Glu Tyr Gly Thr Val Arg Lys Leu Asp Val Thr Pro Ile
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Arg Ile Leu Ala Lys Glu Glu Arg Lys Val Val Cys Asp Asn Asn Pro
 370 375 380

Ile Ser Leu Asn Cys Cys Ser Glu Asn Ile Ala Asn Trp Ser Arg Ile
 385 390 400

Glu Trp Lys Gln Glu Gly Lys Ile Asn Ile Glu Gly Thr Pro Glu Thr
 405 410 415

Asp Leu Glu Ser Ser Cys Ser Thr Tyr Thr Leu Lys Ala Asp Gly Thr
 420 425 430

Gln Cys Pro Ser Gly Ser Ser Gly Thr Thr Val Ile Tyr Thr Cys Glu
 435 440 445

Phe Val Ser Val Tyr Gly Ala Lys Gly Ser Lys Asn Ile Ala Val Thr
 450 455 460

Phe Thr Ser Val Ala Asn Leu Thr Ile Thr Pro Asp Pro Ile Ser Val
 465 470 475 480

Ser Glu Gly Gln Ser Phe Ser Ile Thr Cys Leu Ser Asp Val Ser Ser
 485 490 495

Phe Asp Glu Val Tyr Trp Asn Thr Ser Ala Gly Ile Lys Ile His Pro
 500 505 510

Arg Phe Tyr Thr Met Arg Arg Tyr Arg Asp Gly Ala Glu Ser Val Leu
 515 520 525

Thr Val Lys Thr Ser Thr Arg Glu Trp Asn Gly Thr Tyr His Cys Ile
 530 535 540

Phe Arg Tyr Lys Asn Ser Tyr Ser Ile Ala Thr Lys Asp Val Thr Val
 545 550 555 560

His Pro Leu Pro Leu Glu Ser Asp Ile Met Met Asp Pro Leu Glu Ala
 565 570 575

Ser Gly Leu Cys Thr Ser Ser His Gln Phe Lys Cys Cys Ile Glu Glu
 580 585 590

60.US2.PCT.txt

Asn Asp Gly Glu Glu Tyr Ile Val Thr Phe His Val Asp Ser Ser Ser
595 600 605

Phe Pro Ala Glu Arg Glu Val Ile Gly Lys Gln Ala Cys Tyr Thr Tyr
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Ser Leu Pro Gly Lys Leu Pro Ser Arg Cys Pro Lys Asp Ile Asp Val
625 630 635 640

Phe Cys His Phe Thr Asn Ala Ala Asn Ser Ser Val Arg Ser Pro Ser
645 650 655

Met Lys Leu Thr Leu Val Pro Gly Lys Asn Ile Thr Cys Gln Asp Pro
660 665 670

Ile Ile Gly Ile Gly Glu Pro Gly Lys Val Ile Gln Lys Leu Cys Gln
675 680 685

Phe Ala Gly Val Ser Arg Ser Pro Gly Gln Thr Ile Gly Gly Thr Val
690 695 700

Thr Tyr Lys Cys Val Gly Ser Gln Trp Lys Glu Glu Thr Arg Ala Cys
705 710 715 720

Ile Ser Ala Pro Ile Asn Gly Leu Leu Gln Leu Ala Lys Ala Leu Ile
725 730 735

Lys Ser Pro Ser Gln Asp Gln Lys Leu Pro Lys Tyr Leu Arg Asp Leu
740 745 750

Ser Val Ser Thr Gly Lys Glu Glu Gln Asp Ile Arg Ser Ser Pro Gly
755 760 765

Ser Leu Gly Ala Ile Ile Ser Ile Leu Asp Leu Leu Ser Thr Val Pro
770 775 780

Thr Gln Val Asn Ser Glu Met Met Arg Asp Ile Leu Ala Thr Ile Asn
785 790 795 800

Val Ile Leu Asp Lys Ser Thr Leu Asn Ser Trp Glu Lys Leu Leu Gln
805 810 815

Gln Gln Ser Asn Gln Ser Ser Gln Phe Leu Gln Ser Val Glu Arg Phe
820 825 830

Ser Lys Ala Leu Glu Leu Gly Asp Ser Thr Pro Pro Phe Leu Phe His
Page 14

835

840

845

Pro Asn Val Gln Met Lys Ser Met Val Ile Lys Arg Gly His Ala Gln
 850 855 860

Met Tyr Gln Gln Lys Phe Val Phe Thr Asp Ser Asp Leu Trp Gly Asp
 865 870 875 880

Val Ala Ile Asp Glu Cys Gln Leu Gly Ser Leu Gln Pro Asp Ser Ser
 885 890 895

Ile Val Thr Val Ala Phe Pro Thr Leu Lys Ala Ile Leu Ala Gln Asp
 900 905 910

Gly Gln Arg Lys Thr Pro Ser Asn Ser Leu Val Met Thr Thr Thr Val
 915 920 925

Ser His Asn Ile Val Lys Pro Phe Arg Ile Ser Met Thr Phe Lys Asn
 930 935 940

Asn His Arg Ser Gly Gly Lys Pro Gln Cys Val Phe Trp Asn Phe Ser
 945 950 955 960

Leu Ala Asn Asn Thr Gly Gly Trp Asp Ser Ser Gly Cys Thr Val Glu
 965 970 975

Asp Asp Gly Arg Asp Asn Arg Asp Arg Val Phe Cys Lys Cys Asn His
 980 985 990

Leu Thr Ser Phe Ser Ile Leu Met Ser Pro Asp Ser Pro Asp Pro Gly
 995 1000 1005

Ser Leu Leu Lys Ile Leu Leu Asp Ile Ile Ser Tyr Ile Gly Leu
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Gly Phe Ser Ile Val Ser Leu Ala Ala Cys Leu Val Val Glu Ala
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Met Val Trp Lys Ser Val Thr Lys Asn Arg Thr Ser Tyr Met Arg
 1040 1045 1050

His Ile Cys Ile Val Asn Ile Ala Leu Cys Leu Leu Ile Ala Asp
 1055 1060 1065

Ile Trp Phe Ile Val Ala Gly Ala Ile His Asp Gly His Tyr Pro
 1070 1075 1080

Leu Asn Glu Thr Ala Cys Val Ala Ala Thr Phe Phe Ile His Phe
 1085 1090 1095

Phe Tyr Leu Ser Val Phe Phe Trp Met Leu Thr Leu Gly Leu Met
 1100 1105 1110

Leu Phe Tyr Arg Leu Ile Phe Ile Leu His Asp Ala Ser Lys Ser
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Thr Gln Lys Ala Ile Ala Phe Ser Leu Gly Tyr Gly Cys Pro Leu
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Ile Ile Ser Ser Ile Thr Val Gly Val Thr Gln Pro Gln Glu Val
 1145 1150 1155

Tyr Met Arg Lys Asn Ala Cys Trp Leu Asn Trp Glu Asp Thr Arg
 1160 1165 1170

Ala Leu Leu Ala Phe Ala Ile Pro Ala Leu Ile Ile Val Val Val
 1175 1180 1185

Asn Val Ser Ile Thr Val Val Val Ile Thr Lys Ile Leu Arg Pro
 1190 1195 1200

Ser Val Gly Asp Lys Pro Gly Lys Gln Glu Lys Ser Ser Leu Phe
 1205 1210 1215

Gln Ile Ser Lys Ser Ile Gly Val Leu Thr Pro Leu Leu Gly Leu
 1220 1225 1230

Thr Trp Gly Phe Gly Leu Ala Thr Val Ile Gln Gly Ser Asn Ala
 1235 1240 1245

Val Phe His Ile Ile Phe Thr Leu Leu Asn Ala Phe Gln Gly Leu
 1250 1255 1260

Phe Ile Leu Leu Phe Gly Cys Leu Trp Asp Gln Lys Val Gln Glu
 1265 1270 1275

Ala Leu Leu His Lys Phe Ser Leu Ser Arg Trp Ser Ser Gln His
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Ser Lys Ser Thr Ser Leu Gly Ser Ser Thr Pro Val Phe Ser Met
 1295 1300 1305

Ser Ser Pro Ile Ser Arg Arg Phe Asn Asn Leu Phe Gly Lys Thr
 1310 1315 1320

60.US2.PCT.txt

Gly Thr Tyr Asn Val Ser Thr Pro Glu Thr Thr Ser Ser Ser Val
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Glu Asn Ser Ser Ser Ala Tyr Ser Leu Leu Asn
 1340 1345

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 attgtggctg gtgctatcca cgacggctgc taccactca acgaaacagc ctgtgtggcc 180
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 gccatcgcat tttctctagg ctatggctgt cccctcatta tctcctctat cacagtgggg 360
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 acc 423

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Arg Thr Ser Tyr Met Arg His Ile Cys Ile Val Asn Ile Ala Phe Cys
 20 25 30

Leu Leu Ile Ala Asp Ile Trp Phe Ile Val Ala Gly Ala Ile His Asp
 35 40 45

Gly Arg Tyr Pro Leu Asn Glu Thr Ala Cys Val Ala Ala Thr Phe Phe
 50 55 60

Ile His Phe Phe Tyr Leu Ser Val Phe Phe Trp Met Leu Thr Leu Gly
 65 70 75 80

Leu Met Leu Phe Tyr Arg Leu Ile Phe Ile Leu His Asp Ala Ser Lys
 85 90 95

60.US2.PCT.txt

Ser Thr Gln Lys Ala Ile Ala Phe Ser Leu Gly Tyr Gly Cys Pro Leu
100 105 110

Ile Ile Ser Ser Ile Thr Val Gly Val Thr Gln Pro Gln Glu Val Tyr
115 120 125

Met Arg Lys Asn Ala Cys Trp Leu Asn Trp Glu Asp Thr
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24